IT IS CLAIMED:

1. An oligonucleotide analog compound for use in inhibiting replication in mammalian host cells of an RNA virus having a single-stranded, positive-sense RNA genome and selected from from the Flaviviridae, Picornoviridae, Caliciviridae, Togaviridae, or Coronaviridae families and hepatitis E virus, and characterized by:

(i) a nuclease-resistant backbone,

(ii) capable of uptake by mammalian host cells,

(iii) containing between 12-40 nucleotide bases,

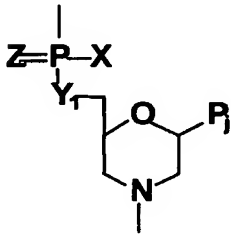
(iv) having a targeting sequence of at least 12 subunits that is complementary to a region associated with stem-loop secondary structure within the 3'-terminal end 40 bases of the negative-sense RNA strand of the virus, and

(v) capable of forming with the negative-strand viral ssRNA genome, a heteroduplex structure having a Tm of dissociation of at least 45 °C and disruption of said stem-loop secondary structure.

2. The compound of claim 1, composed of morpholino subunits linked by uncharged, phosphorus-containing intersubunit linkages, joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit.

3. The compound of claim 2, wherein said intersubunit linkages are phosphorodiamidate linkages.

4. The compound of claim 3, wherein said morpholino subunits are joined by phosphorodiamidate linkages, in accordance with the structure:



where Y_1=O, Z=O, Pj is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide, and X is alkyl, alkoxy, thioalkoxy, or alkyl amino.

5. The compound of claim 4, wherein X=NR_2, where each R is independently hydrogen or methyl.

6. The compound of claim 2, wherein said oligomer has a T_m, with respect to binding to said viral target sequence, of greater than about 50 °C, and said compound is actively taken up by mammalian cells.

7. The compound of claim 1, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:

(i) SEQ ID NO. 1, for St Louis encephalitis virus;
(ii) SEQ ID NO. 2, for Japanese encephalitis virus;
(iii) SEQ ID NO. 3, for a Murray Valley encephalitis virus;
(iv) SEQ ID NO. 4, for a West Nile fever virus;
(v) SEQ ID NO. 5, for a Yellow fever virus
(vi) SEQ ID NO. 6, for a Dengue type 2 virus; and
(vi) SEQ ID NO. 7, for a Hepatitis C virus.

8. The compound of claim 1, directed against a member of the Picornaviridae, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:

(i) SEQ ID NO. 8, for a polio virus of the Mahoney and Sabin strains;
(ii) SEQ ID NO. 9, for a Human enterovirus A;
(iii) SEQ ID NO. 10, for a Human enterovirus B;
(iv) SEQ ID NO. 11, for a Human enterovirus C;
(v) SEQ ID NO. 12, for a Human enterovirus D;
(vi) SEQ ID NO. 13, for a Human enterovirus E;

(vii) SEQ ID NO. 14, for a Bovine enterovirus;
(viii) SEQ ID NO. 15, for Human rhinovirus 89;
(ix) SEQ ID NO. 16, for Human rhinovirus B;
(x) SEQ ID NO. 17, for Foot-and-mouth disease virus; and
(xi) SEQ ID NO. 18, for a hepatitis A virus,

9. The compound of claim 1, directed against member of the Caliciviridae, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:
(i) SEQ ID NO. 19, for Feline Calicivirus;
(ii) SEQ ID NO. 20, for Canine Calicivirus;
(iii) SEQ ID NO. 21, for Porcine enteric calicivirus;
(iv) SEQ ID NO. 22, for Calicivirus strain NB; and
(v) SEQ ID NO. 23, for Norwalk virus.

10. The compound of claim 1, directed against Hepatitis E virus, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence identified as SEQ ID NO: 24.

11. The compound of claim 1, directed against a member of the Togaviridae, Rubella virus, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence identified as SEQ ID NO: 25.

12. The compound of claim 1, directed against member of the Coronaviridae, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:
(i) SEQ ID NO. 26, for SARS coronavirus TOR2;
(ii) SEQ ID NO. 27, for Porcine epidemic diarrhea virus;
(iii) SEQ ID NO. 28, for Transmissible gastroenteritis virus;
(iv) SEQ ID NO. 29, for Bovine coronavirus;

(v) SEQ ID NO. 30, for Human coronavirus 229E. and

(vi) SEQ ID NO. 31, for Murine hepatitis virus.

13. The compound of claim 1, complexed with a complementary-sequence at the 3'-end region of the negative-strand RNA of the virus.

14. A method of inhibiting, in a mammalian host cell, replication of an RNA virus from the Flaviviridae, Picornoviridae, Caliciviridae, Togaviridae, Coronaviridae families and hepatitis E virus, said virus having a single-stranded, positive-sense genome, said method comprising

(a) exposing the host cells to an oligonucleotide analog compound characterized by:

(i) a nuclease-resistant backbone,

(ii) capable of uptake by mammalian host cells,

(iii) containing between 12-40 nucleotide bases, and

(iv) having a targeting sequence of at least 12 subunits that is complementary to a region associated with stem-loop secondary structure within the 3'-terminal end 40 bases of the negative-sense RNA strand of the virus, and

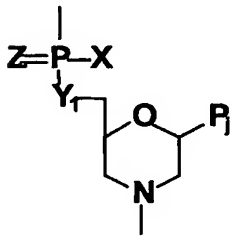
(b) by said exposing, forming within said cells a heteroduplex structure composed of the negative sense strand of the virus and the oligonucleotide compound, and characterized by a Tm of dissociation of at least 45 °C and disruption of said stem-loop secondary structure.

15. The method of claim 14, wherein said oligonucleotide is administered to a mammalian subject infected with said virus, or at risk of infection with said virus.

16. The method of claim 15, wherein said oligonucleotide is composed of morpholino subunits linked by uncharged, phosphorus-containing intersubunit linkages, joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit.

17. The method of claim 16, wherein said intersubunit linkages are phosphorodiamidate linkages.

18. The method of claim 17, wherein said morpholino subunits are joined by phosphorodiamidate linkages, in accordance with the structure:



where Y_1=O, Z=O, Pj is a purine or pyrimidine base-pairing moiety effective to bind, by base-specific hydrogen bonding, to a base in a polynucleotide, and X is alkyl, alkoxy, thioalkoxy, or alkyl amino.

19. The method of claim 18, wherein X=NR_2, where each R is independently hydrogen or methyl.

20. The method of claim 17, wherein said compound is administered orally to a mammalian subject infected with the virus or at risk of infection with the virus.

21. The compound of claim 14, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:

(i) SEQ ID NO. 1, for St Louis encephalitis virus;
(ii) SEQ ID NO. 2, for Japanese encephalitis virus;
(iii) SEQ ID NO. 3, for a Murray Valley encephalitis virus;
(iv) SEQ ID NO. 4, for a West Nile fever virus;
(v) SEQ ID NO. 5, for a Yellow fever virus
(vi) SEQ ID NO. 6, for a Dengue type 2 virus; and
(vii) SEQ ID NO. 7, for a Hepatitis C virus.

22. The method of claim 14, directed against a member of the Picornaviridae, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:

(i) SEQ ID NO. 8, for a polio virus of the Mahoney and Sabin strains;
(ii) SEQ ID NO. 9, for a Human enterovirus A;
(iii) SEQ ID NO. 10, for a Human enterovirus B;
(iv) SEQ ID NO. 11, for a Human enterovirus C;
(v) SEQ ID NO. 12, for a Human enterovirus D;
(vi) SEQ ID NO. 13, for a Human enterovirus E;
(vii) SEQ ID NO. 14, for a Bovine enterovirus;
(viii) SEQ ID NO. 15, for Human rhinovirus 89;
(ix) SEQ ID NO. 16, for Human rhinovirus B;
(x) SEQ ID NO. 17, for Foot-and-mouth disease virus; and
(xi) SEQ ID NO. 18, for a hepatitis A virus,

23. The method of claim 14, directed against member of the Caliciviridae, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:

(i) SEQ ID NO. 19, for Feline Calicivirus;
(ii) SEQ ID NO. 20, for Canine Calicivirus;
(iii) SEQ ID NO. 21, for Porcine enteric calicivirus;
(iv) SEQ ID NO. 22, for Calicivirus strain NB; and
(v) SEQ ID NO. 23, for Norwalk virus.

24. The method of claim 14, directed against Hepatitis E virus, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence identified as SEQ ID NO: 24.

25. The method of claim 14, directed against a member of the Togaviridae, Rubella virus, wherein said targeting sequence is complementary to

a region associated with stem-loop secondary structure within the sequence identified as SEQ ID NO: 25.

26. The method of claim 13, directed against member of the Coronaviridae, wherein said targeting sequence is complementary to a region associated with stem-loop secondary structure within the sequence selected from the group consisting of:

(i) SEQ ID NO. 26, for SARS coronavirus TOR2;

(ii) SEQ ID NO. 27, for Porcine epidemic diarrhea virus;

(iii) SEQ ID NO. 28, for Transmissible gastroenteritis virus;

(iv) SEQ ID NO. 29, for Bovine coronavirus;

(v) SEQ ID NO. 30, for Human coronavirus 229E. and

(vi) SEQ ID NO. 31, for Murine hepatitis virus.

27. A method of confirming the presence of an effective interaction between a picornavirus, calicivirus, togavirus, coronavirus, hepatitis E virus, or flavivirus infecting a mammalian subject, and an uncharged morpholino sense oligonucleotide analog compound against the infecting virus, comprising

(a) administering said compound to the subject, where said compound has (a) a sequence of 12-40 subunits, including a targeting sequence of at least 12 subunits that is complementary to a region associated with stem-loop secondary structure within the 3'-terminal end 40 bases of the negative-sense RNA strand of the virus, (b) morpholino subunits linked by uncharged, phosphorus-containing intersubunit linkages, each linkage joining a morpholino nitrogen of one subunit to a 5' exocyclic carbon of an adjacent subunit, and (c) is capable of forming with the negative-strand viral ssRNA genome, a heteroduplex structure characterized by a Tm of dissociation of at least 45 °C and disruption of said stem-loop secondary structure,

(b) at a selected time after said administering, obtaining a sample of a body fluid from the subject; and

(c) assaying the sample for the presence of a nuclease-resistant heteroduplex comprising the sense oligonucleotide complexed with a

complementary-sequence 3'-end region of the negative-strand RNA of the virus.

28. The method of claim 27, wherein the linkages are phosphorodiamidate linkages.

29. The method of claim 27, for use in determining the effectiveness of treating a picornavirus, calicivirus, togavirus, coronavirus, hepatitis E virus or flavivirus infection by administering said oligomer, wherein said administering, obtaining, and assaying is conducted at periodic intervals throughout a treatment period.